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SEQUENCE LISTING

16
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WATAHIKI, Masanori

<120> RNA Polymerase

<130> 024705-077

<140> US 09/254,344
<141> 1999-09-03

<150> PCT/JP98/03037
<151> 1998-07-06

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<170> PatentIn version 3.0

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51

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Glu Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu
15 20 25 30

99

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Arg Leu Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met
35 40 45

147

ggt gaa gca cgc ttc cgc aag atg ttt gag cgt caa ctt aaa gct ggt
Gly Glu Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly
50 55 60

195

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Glu Val Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu
65 70 75

243

cct aag atg att gca cgc atc aac gac tgg ttt gag gaa gtg aaa gct

291

Pro Lys Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala			
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Lys Arg Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys			
95	100	105	110
ccg gaa gcc gta gcg tac atc acc att aag acc act ctg gct tgc cta			387
Pro Glu Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu			
115	120	125	
acc agt gct gac aat aca acc gtt cag gct gta gca agc gca atc ggt			435
Thr Ser Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly			
130	135	140	
cgg gcc att gag gac gag gct cgc ttc ggt cgt atc cgt gac ctt gaa			483
Arg Ala Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu			
145	150	155	
gct aag cac ttc aag aaa aac gtt gag gaa caa ctc aac aag cgc gta			531
Ala Lys His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val			
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ggg cac gtc tac aag aaa gca ttt atg caa gtt gtc gag gct gac atg			579
Gly His Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met			
175	180	185	190
ctc tct aag ggt cta ctc ggt ggc gag gcg tgg tct tcg tgg cat aag			627
Leu Ser Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys			
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gaa gac tct att cat gta gga gta cgc tgc atc gag atg ctc att gag			675
Glu Asp Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu			
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tca acc gga atg gtt agc tta cac cgc caa aat gct ggc gta gta ggt			723
Ser Thr Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly			
225	230	235	
caa gac tct gag act atc gaa ctc gca cct gaa tac gct gag gct atc			771
Gln Asp Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile			
240	245	250	
gca acc cgt gca ggt gcg ctg gct ggc atc tct ccg atg ttc caa cct			819
Ala Thr Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro			
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tgc gta gtt cct cct aag ccg tgg act ggc att act ggt ggt ggc tat			867
Cys Val Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr			
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tgg gct aac ggt cgt cgt cct ctg gcg ctg gtg cgt act cac agt aag			915
Trp Ala Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys			
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aaa gca ctg atg cgc tac gaa gac gtt tac atg cct gag gtg tac aaa			963
Lys Ala Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys			

305	310	315	
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cta gcg gtc gcc aac gta atc acc aag tgg aag cat tgt ccg gtc gag Leu Ala Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu 335	340	345	1059
gac atc cct gcg att gag cgt gaa gaa ctc ccg atg aaa ccg gaa gac Asp Ile Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp 355	360	365	1107
atc gac atg aat cct gag gct ctc acc gcg tgg aaa cgt gct gcc gct Ile Asp Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala 370	375	380	1155
gct gtg tac cgc aag gac aag gct cgc aag tct cgc cgt atc, agc ctt Ala Val Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu 385	390	395	1203
gag ttc atg ctt gag caa gcc aat aag ttt gct aac cat aag gcc atc Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile 400	405	410	1251
tgg ttc cct tac aac atg gac tgg cgc ggt cgt gtt tac gct gtg tca Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser 415	420	425	1299
atg ttc aac ccg caa ggt aac gat atg acc aaa gga ctg ctt acg ctg Met Phe Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu 435	440	445	1347
gcg aaa ggt aaa cca atc ggt aag gaa ggt tac tac tgg ctg aaa atc Ala Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile 450	455	460	1395
cac ggt gca aac tgt gcg ggt gtc gat aag gtt ccg ttc cct gag cgc His Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg 465	470	475	1443
atc aag ttc att gag gaa aac cac gag aac atc atg gct tgc gct aag Ile Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys 480	485	490	1491
tct cca ctg gag aac act tgg tgg gct gag caa gat tct ccg ttc tgc Ser Pro Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys 495	500	505	1539
ttc ctt gcg ttc tgc ttt gag tac gct ggg gta cag cac cac ggc ctg Phe Leu Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu 515	520	525	1587
agc tat aac tgc tcc ctt ccg ctg gcg ttt gac ggg tct tgc tct ggc Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly 530	535	540	1635

atc cag cac ttc tcc gcg atg ctc cga gat gag gta ggt ggt cgc gcg Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala 545 550 555	1683
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gag aaa gtc aag ctg ggc act aag gca ctg gct ggt caa tgg ctg gct Glu Lys Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala 610 615 620	1875
tac ggt gtt act cgc agt gtg act aag cgt tca gtc atg acg ctg gct Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala 625 630 635	1923
tac ggg tcc aaa gag ttc ggc ttc cgt caa caa gtg ctg gaa gat acc Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr 640 645 650	1971
att cag cca gct att gat tcc ggc aag ggt ctg atg ttc act cag ccg Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro 655 660 665 670	2019
aat cag gct ggt gga tac atg gct aag ctg att tgg gaa tct gtg agc Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser 675 680 685	2067
gtg acg gtg gta gct gcg gtt gaa gca atg aac tgg ctt aag tct gct Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala 690 695 700	2115
gct aag ctg ctg gct gag gtc aaa gat aag aag act gga gag att Ala Lys Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile 705 710 715	2163
ctt cgc aag cgt tgc gct gtg cat tgg gta act cct gat ggt ttc cct Leu Arg Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro 720 725 730	2211
gtg tgg cag gaa tac aag aag cct att cag acg cgc ttg aac ctg atg Val Trp Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met 735 740 745 750	2259
tcc ctc ggt cag ttc cgc tta cag cct acc att aac acc aac aaa gat Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp 755 760 765	2307
agc gag att gat gca cac aaa cag gag tct ggt atc gct cct aac ttt	2355

Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe			
770	775	780	
gta cac agc caa gac ggt agc cac ctt cgt aag act gta gtg tgg gca		2403	
Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala			
785	790	795	
cac gag aag tac gga atc gaa tct ttt gca ctg att cac gac tcc ttc		2451	
His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe			
800	805	810	
ggt acc att ccg gct gac gct gcg aac ctg ttc aaa gca gtg cgc gaa		2499	
Gly Thr Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu			
815	820	825	830
act atg gtt gac aca tat gag tct tgt gat gta ctg gct gat ttc tac		2547	
Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr			
835	840	845	
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Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro			
850	855	860	
gca ctt ccg gct aaa ggt aac ttg aac ctc cgt gac atc tta gag tcg		2643	
Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser			
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20	25	30	
Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu			
35	40	45	
Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val			
50	55	60	
Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys			
65	70	75	80

Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
 85 90 95

Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
 100 105 110

Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
 115 120 125

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
 130 135 140

Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
 145 150 155 160

His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
 165 170 175

Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
 180 185 190

Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
 195 200 205

Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
 210 215 220

Gly Met Val Ser Leu His Arg Gln Asn Ala Gly Val Val Gly Gln Asp
 225 230 235 240

Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
 245 250 255

Arg Ala Gly Ala Leu Ala Gly Ile Ser Pro Met Phe Gln Pro Cys Val
 260 265 270

Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Tyr Trp Ala
 275 280 285

Asn Gly Arg Arg Pro Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala
 290 295 300

Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val Tyr Lys Ala Ile

305

310

315

320

Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys Lys Val Leu Ala
 325 330 335

Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
 340 345 350

Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro Glu Asp Ile Asp
 355 360 365

Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala Ala Ala Ala Val
 370 375 380

Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile Ser Leu Glu Phe
 385 390 395 400

Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe
 405 410 415

Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
 420 425 430

Asn Pro Gln Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala Lys
 435 440 445

Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His Gly
 450 455 460

Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile Lys
 465 470 475 480

Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser Pro
 485 490 495

Leu Glu Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Cys Phe Leu
 500 505 510

Ala Phe Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr
 515 520 525

Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln
 530 535 540

His Phe Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn
545 550 555 560

Leu Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys
565 570 575

Lys Val Asn Glu Ile Leu Gln Ala Asp Ala Ile Asn Gly Thr Asp Asn
580 585 590

Glu Val Val Thr Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys
595 600 605

Val Lys Leu Gly Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly
610 615 620

Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly
625 630 635 640

Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln
645 650 655

Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
660 665 670

Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
675 680 685

Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
690 695 700

Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Thr Gly Glu Ile Leu Arg
705 710 715 720

Lys Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp
725 730 735

Gln Glu Tyr Lys Lys Pro Ile Gln Thr Arg Leu Asn Leu Met Phe Leu
740 745 750

Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu
755 760 765

Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His
 770 775 780

Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
 785 790 795 800

Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr
 805 810 815

Ile Pro Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met
 820 825 830

Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 835 840 845

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
 850 855 860

Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser Asp Phe
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Ala Phe Ala

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Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu
 35 40 45

Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Lys Met Ile Ala
 65 70 75 80

Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg Gly Lys Arg
 85 90 95

Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu Ala Val Ala

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Tyr Ile Thr Ile Lys Thr Thr	Leu Ala Cys Leu Thr Ser Ala Asp Asn	
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Thr Thr Val Gln Ala Ala Ile Gly Arg Ala Ile Glu Asp Glu Ala Arg		
130	135	140
Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys His Phe Lys Lys Asn Val		
145	150	155
Glu Glu Gln Leu Asn Lys Arg Val Gly His Val Tyr Lys Lys Ala Phe		
165	170	175
Met Gln Val Val Glu Ala Asp Met Leu Ser Lys Gly Leu Leu Gly Gly		
180	185	190
Glu Ala Trp Ser Ser Trp His Lys Glu Asp Ser Ile His Val Gly Val		
195	200	205
Arg Met Leu Ile Glu Ser Thr Gly Met Val Ser Leu His Arg Gln Asn		
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Ala Gly Val Val Gly Gln Asp Ser Glu Thr Ile Glu Leu Ala Pro Glu		
225	230	235
Tyr Ala Glu Ala Ile Ala Thr Arg Ala Gly Ala Leu Ala Gly Ile Ser		
245	250	255
Pro Met Phe Gln Pro Cys Val Val Pro Pro Lys Pro Trp Thr Gly Ile		
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Thr Gly Gly Tyr Trp Ala Asn Gly Leu Ala Leu Val Arg Thr His		
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Ser Lys Lys Ala Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val		
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Tyr Lys Ala Ile Asn Ile Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys		
305	310	320
Lys Val Leu Ala Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro		
325	330	335
Val Glu Asp Ile Pro Ala Ile Glu Arg Glu Glu Leu Pro Met Lys Pro		
340	345	350
Glu Asp Ile Asp Met Asn Pro Glu Ala Leu Thr Ala Trp Lys Arg Ala		
355	360	365
Ala Ala Ala Val Tyr Arg Lys Asp Lys Ala Arg Lys Ser Arg Arg Ile		
370	375	380
Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Asn His Lys		
385	390	400
Ala Ile Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala		

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420	425	430	
Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr Tyr Trp Leu Lys Ile His			
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Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile			
450	455	460	
Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser			
465	470	475	480
Pro Leu Glu Asn Thr Ile Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala			
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Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln His			
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Leu Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Lys Lys			
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Val Asn Glu Ile Leu Gln Ala Asn Gly Thr Asp Asn Glu Val Val Thr			
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Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys Val Lys Leu Gly			
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Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser			
595	600	605	
Val Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe			
610	615	620	
Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp			
625	630	635	640
Ser Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys			
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Leu Ile Trp Glu Ser Val Ser Val Thr Val Val Ala Ala Val Glu Ala			
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Met Asn Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys			
675	680	685	
Asp Lys Lys Thr Gly Glu Ile Leu Arg Lys Arg Cys Ala Val His Trp			
690	695	700	
Val Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Ile Gln Thr Arg			

705	710	715	720
Leu Asn Leu Met Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn			
725		730	735
Thr Asn Lys Asp Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile			
740		745	750
Ala Pro Asn Phe Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr			
755		760	765
Val Val Trp Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile			
770		775	780
His Asp Ser Phe Gly Thr Ile Pro Ala Asn Leu Phe Lys Ala Val Arg			
785		790	795
Glu Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe			
805		810	815
Tyr Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met			
820		825	830
Pro Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu			
835		840	845
Ser Asp Phe Ala Phe Ala			
850			

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20		25	30
Leu Ala Lys Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Leu Gly			
35	40	45	
Glu Arg Arg Phe Leu Lys Met Leu Glu Arg Gln Ala Lys Ala Gly Glu			
50	55	60	
Ile Ala Asp Asn Ala Ala Lys Pro Leu Leu Ala Thr Lys Leu Thr			
65	70	75	80
Thr Arg Ile Val Glu Trp Leu Glu Glu Tyr Ala Ser Lys Lys Gly Arg			
85		90	95
Lys Pro Ser Ala Tyr Ala Pro Leu Gln Leu Leu Lys Pro Glu Ala Ser			
100		105	110

Ala Phe Ile Thr Leu Lys Val Ile Leu Ala Ser Leu Thr Ser Thr Asn
 115 120 125
 Met Thr Thr Ile Gln Ala Met Leu Gly Lys Ala Ile Glu Asp Glu Ala
 130 135 140
 Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys His Phe Lys Lys His
 145 150 155 160
 Val Glu Glu Gln Leu Asn Lys Arg His Gly Gln Val Tyr Lys Lys Ala
 165 170 175
 Phe Met Gln Val Val Glu Ala Asp Met Ile Gly Arg Gly Leu Leu Gly
 180 185 190
 Gly Glu Ala Trp Ser Ser Trp Asp Lys Glu Thr Thr Met His Val Gly
 195 200 205
 Ile Arg Met Leu Ile Glu Ser Thr Gly Leu Val Glu Leu Gln Arg His
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 Asn Ala Gly Asn Ala Gly Ser Asp His Glu Ala Leu Gln Leu Ala Gln
 225 230 235 240
 Glu Tyr Val Asp Val Leu Ala Lys Ala Gly Ala Leu Ala Gly Ile Ser
 245 250 255
 Pro Met Phe Gln Pro Cys Val Val Pro Pro Lys Pro Trp Val Ala Ile
 260 265 270
 Thr Gly Gly Tyr Trp Ala Asn Gly Leu Ala Leu Val Arg Thr His
 275 280 285
 Ser Lys Lys Gly Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val
 290 295 300
 Tyr Lys Ala Val Asn Leu Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys
 305 310 315 320
 Lys Val Leu Ala Val Val Asn Glu Ile Val Asn Trp Lys Asn Cys Pro
 325 330 335
 Val Ala Asp Ile Pro Ser Leu Glu Arg Gln Glu Leu Pro Pro Lys Pro
 340 345 350
 Asp Asp Ile Asp Thr Asn Glu Ala Ala Leu Lys Glu Trp Lys Lys Ala
 355 360 365
 Ala Ala Gly Ile Tyr Arg Leu Asp Lys Ala Arg Val Ser Arg Arg Ile
 370 375 380
 Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Ser Lys Lys
 385 390 395 400
 Ala Ile Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala
 405 410 415

Val Pro Met Phe Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala
 420 425 430
 Lys Gly Lys Pro Ile Gly Glu Glu Gly Phe Tyr Trp Leu Lys Ile His
 435 440 445
 Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile
 450 455 460
 Ala Phe Ile Glu Lys His Val Asp Asp Ile Leu Ala Cys Ala Lys Asp
 465 470 475 480
 Pro Ile Asn Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala Phe
 485 490 495
 Cys Phe Glu Tyr Ala Gly Val Thr His His Gly Leu Ser Tyr Asn Cys
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 Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln His Phe
 515 520 525
 Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn Leu Leu
 530 535 540
 Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Gln Lys Val
 545 550 555 560
 Asn Glu Ile Leu Lys Gln Asn Gly Thr Pro Asn Glu Met Ile Thr Val
 565 570 575
 Thr Asp Lys Asp Thr Gly Glu Ile Ser Glu Lys Leu Lys Leu Gly Thr
 580 585 590
 Ser Thr Leu Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val
 595 600 605
 Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly
 610 615 620
 Phe Arg Gln Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser
 625 630 635 640
 Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 645 650 655
 Ile Trp Asp Ala Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met
 660 665 670
 Asn Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp
 675 680 685
 Lys Lys Thr Lys Glu Ile Leu Arg His Arg Cys Ala Val His Trp Thr
 690 695 700
 Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Leu Gln Lys Arg Leu
 705 710 715 720

Asp Met Ile Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr
 725 730 735
 Leu Lys Asp Ser Gly Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala
 740 745 750
 Pro Asn Phe Val His Ser Gln Asp Gly Ser Arg Leu Met Thr Val Val
 755 760 765
 Tyr Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp
 770 775 780
 Ser Phe Gly Thr Ile Pro Gly Lys Leu Phe Lys Ala Val Arg Glu Thr
 785 790 795 800
 Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser
 805 810 815
 Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro
 820 825 830
 Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp
 835 840 845
 Phe Ala Phe Ala
 850

<210> 5
 <211> 876
 <212> PRT
 <213> Bacteriophage K11

<400> 5
 Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu
 1 5 10 15
 Ala Ala Ile Pro Tyr Asn Ile Leu Ser Glu His Tyr Gly Asp Gln Ala
 20 25 30
 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ala Tyr Glu Leu Gly Arg
 35 40 45
 Gln Arg Phe Leu Lys Met Leu Glu Arg Gln Val Lys Ala Gly Glu Phe
 50 55 60
 Ala Asp Asn Ala Ala Lys Pro Leu Val Leu Thr Gln Leu Thr Lys
 65 70 75 80
 Arg Ile Asp Asp Trp Lys Glu Glu Gln Ala Asn Ala Arg Gly Lys Lys
 85 90 95
 Pro Arg Ala Tyr Tyr Pro Ile Lys His Gly Val Ala Ser Glu Leu Ala
 100 105 110
 Val Ser Met Gly Ala Glu Val Leu Lys Glu Lys Arg Gly Val Ser Ser
 115 120 125

Glu Ala Ile Ala Leu Leu Thr Ile Lys Val Val Leu Gly Asn Ala His
 130 135 140
 Arg Pro Leu Lys Gly His Asn Pro Ala Gln Leu Gly Lys Ala Leu Glu
 145 150 155 160
 Asp Glu Ala Arg Phe Gly Arg Ile Arg Glu Gln Glu Ala Ala Tyr Phe
 165 170 175
 Lys Lys Asn Val Ala Asp Gln Leu Asp Lys Arg Val Gly His Val Tyr
 180 185 190
 Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Ile Ser Lys Gly
 195 200 205
 Met Leu Gly Gly Asp Asn Trp Ala Ser Trp Lys Thr Asp Glu Gln Met
 210 215 220
 His Val Gly Thr Lys Leu Leu Ile Glu Gly Thr Gly Leu Val Glu Met
 225 230 235 240
 Thr Lys Asn Lys Met Ala Asp Gly Ser Asp Asp Val Thr Ser Met Gln
 245 250 255
 Met Val Gln Leu Ala Pro Ala Phe Val Glu Leu Leu Ser Lys Arg Ala
 260 265 270
 Gly Ala Leu Ala Gly Ile Ser Pro Met His Gln Pro Cys Val Val Pro
 275 280 285
 Pro Lys Pro Trp Val Glu Thr Val Gly Gly Tyr Trp Ser Val Gly
 290 295 300
 Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala Leu Arg Arg Tyr Ala
 305 310 315 320
 Asp Val His Met Pro Glu Val Tyr Lys Ala Val Asn Leu Ala Gln Asn
 325 330 335
 Thr Pro Trp Lys Val Asn Lys Val Leu Ala Val Val Asn Glu Ile
 340 345 350
 Val Asn Trp Lys His Cys Pro Val Gly Asp Val Pro Ala Ile Glu Arg
 355 360 365
 Glu Glu Leu Pro Pro Arg Pro Asp Asp Ile Asp Thr Asn Glu Val Ala
 370 375 380
 Arg Lys Ala Trp Arg Lys Glu Ala Ala Ala Val Tyr Arg Lys Asp Lys
 385 390 395 400
 Ala Arg Gln Ser Arg Arg Cys Arg Cys Glu Phe Met Val Ala Gln Ala
 405 410 415
 Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp
 420 425 430

Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe Gly Asn Asp Met Thr
 435 440 445
 Lys Gly Ser Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Leu Asp Gly
 450 455 460
 Phe Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys
 465 470 475 480
 Val Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn Glu Gly Asn
 485 490 495
 Ile Leu Ala Ser Ala Ala Asp Pro Leu Asn Thr Trp Trp Thr Gln Gln
 500 505 510
 Asp Ser Pro Phe Ala Phe Cys Phe Glu Tyr Ala Gly Val Lys His His
 515 520 525
 Gly Leu Asn Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser
 530 535 540
 Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly
 545 550 555 560
 Gly Arg Ala Val Asn Leu Leu Pro Ser Asp Thr Val Asp Ile Tyr Lys
 565 570 575
 Ile Val Ala Asp Lys Val Asn Glu Val Leu His Gln Asn Gly Ser Gln
 580 585 590
 Thr Val Val Glu Gln Ile Ala Asp Lys Glu Thr Gly Glu Phe His Glu
 595 600 605
 Lys Val Thr Leu Gly Glu Ser Val Leu Ala Ala Gly Gln Trp Leu Gln
 610 615 620
 Tyr Gly Val Thr Arg Lys Val Thr Lys Arg Ser Val Met Thr Leu Ala
 625 630 635 640
 Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln Gln Val Leu Glu Asp Thr
 645 650 655
 Ile Gln Pro Ala Ile Asp Asn Gly Glu Phe Thr His Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Asp Ala Ser Thr Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Gly Val Ile Leu His
 705 710 715 720
 Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp Gln
 725 730 735

Glu Gln Asn Gln Ala Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn
 740 745 750

Val Lys Met Thr Tyr Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His
 755 760 765

Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 770 775 780

Ser His Leu Arg Met Thr Val Val His Ala Asn Glu Val Tyr Gly Ile
 785 790 795 800

Asp Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro Gly Asn
 805 810 815

Leu Phe Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn
 820 825 830

Asp Val Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu
 835 840 845

Ser Gln Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn
 850 855 860

Leu Arg Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala
 865 870 875

<210> 6

<211> 841

<212> PRT

<213> Bacteriophage SP6

<400> 6

Met Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe
 1 5 10 15

Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala
 20 25 30

Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu
 35 40 45

Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys Glu Glu Tyr Glu Gly Lys
 50 55 60

Lys Gly Arg Ala Pro Arg Ala Leu Ala Phe Leu Gln Cys Val Glu Asn
 65 70 75 80

Glu Val Ala Ala Tyr Ile Thr Met Lys Val Val Met Asp Met Leu Asn
 85 90 95

Thr Asp Ala Thr Leu Gln Ser Val Ala Glu Arg Ile Glu Asp Gln Val
 100 105 110

Arg Phe Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe Glu Lys Val
 115 120 125

Lys Lys Ser Leu Lys Ala Ser Arg Thr Lys Ser Tyr Arg His Ala His
 130 135 140
 Asn Val Ala Val Val Ala Glu Lys Ser Val Ala Glu Lys Asp Ala Asp
 145 150 155 160
 Phe Asp Arg Trp Glu Ala Trp Pro Lys Glu Thr Gln Leu Gln Ile Gly
 165 170 175
 Thr Thr Ile Leu Glu Gly Ser Val Phe Tyr Asn Gly Glu Pro Val Phe
 180 185 190
 Met Arg Ala Met Arg Thr Tyr Gly Gly Lys Thr Ile Tyr Tyr Leu Gln
 195 200 205
 Thr Ser Glu Ser Val Gly Gln Trp Ile Ser Ala Phe Lys Glu His Val
 210 215 220
 Ala Gln Leu Ser Pro Ala Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro
 225 230 235 240
 Trp Arg Thr Pro Phe Asn Gly Gly Phe His Thr Glu Lys Val Ile Arg
 245 250 255
 Leu Val Lys Gly Asn Arg Glu His Val Arg Lys Leu Thr Gln Lys Gln
 260 265 270
 Met Pro Lys Val Tyr Lys Ala Ile Asn Ala Leu Gln Asn Thr Gln Trp
 275 280 285
 Gln Ile Asn Lys Asp Val Leu Ala Val Ile Glu Glu Val Ile Arg Leu
 290 295 300
 Asp Leu Gly Tyr Gly Val Pro Ser Phe Lys Pro Leu Ile Asp Lys Glu
 305 310 315 320
 Asn Lys Pro Ala Asn Pro Val Pro Val Glu Leu Arg Gly Arg Glu Leu
 325 330 335
 Lys Glu Met Leu Ser Pro Glu Gln Trp Gln Gln Phe Ile Asn Trp Lys
 340 345 350
 Gly Glu Cys Ala Arg Leu Tyr Thr Ala Glu Thr Lys Arg Gly Ser Lys
 355 360 365
 Ser Ala Ala Val Val Arg Met Val Gly Gln Ala Arg Lys Tyr Ser Ala
 370 375 380
 Phe Glu Ser Ile Tyr Phe Val Tyr Ala Met Asp Ser Arg Ser Arg Val
 385 390 395 400
 Tyr Val Gln Ser Ser Thr Leu Ser Asn Asp Leu Gly Lys Ala Leu Leu
 405 410 415
 Arg Phe Thr Glu Gly Arg Pro Val Asn Gly Val Glu Ala Leu Lys Trp
 420 425 430

Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys Lys Thr Phe
 435 440 445
 Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln Asp Met Cys
 450 455 460
 Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp Ala Lys Ala
 465 470 475 480
 Asp Ala Pro Tyr Ala Trp Cys Phe Glu Tyr Ala Gln Tyr Leu Asp Leu
 485 490 495
 Val Asp Glu Gly Arg Ala Asp Glu Phe Arg Thr His Leu Pro Val His
 500 505 510
 Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu Arg
 515 520 525
 Asp Glu Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp Ala Pro
 530 535 540
 Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Asn Ala Leu Tyr
 545 550 555 560
 Met Asp Ala Asp Asp Ala Thr Thr Phe Thr Ser Gly Ser Val Thr Leu
 565 570 575
 Ser Gly Thr Glu Leu Arg Ala Met Ala Ser Ala Trp Asp Ser Ile Gly
 580 585 590
 Ile Thr Arg Ser Leu Thr Lys Lys Pro Val Met Thr Leu Pro Tyr Gly
 595 600 605
 Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr Ile Val Asp
 610 615 620
 Leu Glu Glu Lys Glu Ala Gln Lys Glu Gly Arg Thr Ala Asn Lys Val
 625 630 635 640
 His Pro Phe Glu Asp Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 645 650 655
 Tyr Asn Tyr Met Thr Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val
 660 665 670
 Lys Ala Pro Ile Val Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe
 675 680 685
 Ala Ala Lys Arg Asn Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe
 690 695 700
 Ile Leu Glu Gln Lys Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met
 705 710 715 720
 Gly Asp Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu
 725 730 735

Ala Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp
 740 745 750

Ala Ser His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val
 755 760 765

Thr Ser Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Leu Thr
 770 775 780

Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp Gly
 785 790 795 800

Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met Val
 805 810 815

Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu
 820 825 830

Ile Met Asp Ser Glu Tyr Val Phe Ala
 835 840

<210> 7

<211> 78

<212> PRT

<213> Bacteriophage T7

<400> 7

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 8

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F644Y.

<400> 8

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 9

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F646Y.

<400> 9

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 10

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 11
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<400> 11
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 12
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase F644Y.

<400> 12
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 13
<211> 73
<212> PRT
<213> Bacteriophage T7

<220>
<221> PEPTIDE
<222> (1)..(73)
<223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13
Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
35 40 45

Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
65 70

<210> 14
<211> 73
<212> PRT
<213> Bacteriophage T3

<400> 14
Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
20 25 30

Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
50 55 60

Ile Trp Asp Ala Val Ser Val Thr Val
65 70

<210> 15
<211> 73
<212> PRT
<213> Bacteriophage K11

<400> 15
Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly
 35 40 45

Leu Met Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Asp Ala Val Thr Val Thr Val
 65 70

<210> 16

<211> 75

<212> PRT <

213> Bacteriophage SP6

<400> 16

Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys
 1 5 10 15

Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu
 20 25 30

Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys
 35 40 45

Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp
 50 55 60

Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 65 70 75

<210> 17

<211> 31

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(31)

<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc_feature

<222> (25)..(25)

<223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17

gggaggggggg gggggggggcc ccccnngggcg t

31

<210> 18

<211> 32

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(32)

<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc_feature

<222> (1)..(32)

<223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18
gcgtcnnnaa aacgcacntt ttctntcgtn gg 32

<210> 19

<211> 19

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(19)

<223> Mutant T7 RNA polymerase F644Y.

<400> 19
cgaggggggg ccggtagcc 19

<210> 20

<211> 25

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(25)

<223> Mutant T7 RNA polymerase F644Y.

<220>

<221> misc_feature

<222> (6)..(6)

<223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20
cccccttttg ttccttttagt gaggt 25

<210> 21

<211> 18

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

Cont
 16

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<222> (1)..(18)
<223> Mutant T7 RNA polymerase F667Y.

<400> 21
gagggggggcc ggtaacgc 18

<210> 22
<211> 22
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(22)
<223> Mutant T7 RNA polymerase F667Y.

<400> 22
acgccttttg ttccctttag tg 22

<210> 23
<211> 569
<212> DNA
<213> Bacteriophage T7
<220>
<221> misc_feature
<222> (1)..(569)
<223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

<220>
<221> misc_feature
<222> (1)..(472)
<223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7
      5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"
      wherein "n" = any nucleotide

<400> 23
nnnnnnnnnn nnnnggnngt nggttncgna tccnaaangn aacaggggn nantgtgnaa 60
acatgaatat ttttnntaag ctttnattcc agggcaagac attttaaccn aaattgncaa 120
attatatcac tnattagaca gaaaaatctn acccagntaa gacttctgga ggtttggta 180
agtagtttgt cttggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca 240
cacttcagct taaaccaaca ggataggaaa aatagggagc aacatggagt ggcacccctgg 300
tatttctaca gtcctgtaga tgaagtctct atatgtcaa catcctggga cagagcatat 360
ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatggtg 420
tggatgggt tagcaataan cacactctct ctttcgatg tgcattgtat antcaggtgg 480
ataaaaaaaag acatcgcttg gcccacatgc aaggccaaaa agcagacatc agaaagagag 540
cagtcatgtg gggaaattgg tccgactgc 569
  
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B
 Cont